

Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser
 515 520 525
 5 Pro Ala Ala Gly Asp Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe
 530 535 540
 Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln
 545 550 555 560
 10 Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn
 565 570 575
 Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val
 580 585 590
 15 Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe
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 20 Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp
 610 615 620
 Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu
 625 630 635 640
 25 Pro Ser Ala Ala Ile Gly Gly Gly Val Ala Val Gly Glu Pro Val Val
 645 650 655
 Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro
 560 665 670
 30 Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu
 675 680 685
 35 Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala
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 40 Val Val Gly Met Asn Thr Ala Ala Ser
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 45 <210> SEQ ID NO:19
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 <212> DNA
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 <223> Description of Artificial Sequence:bi-fusion
 50 protein TBH9-Ra35 (designated Mtb59f)
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 ccg gag atc aac tcc gcg agg atg tac gcc gcc ccg ggt tcc gcc tcc 56
 Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser Ala Ser
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 60 ctg gcg gcc gcg gct cag atg tgg gac agc gtg gcg agt gac ctg att 144
 Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp Leu Phe
 35 40 45
 65 tcc gcc gcg tcc gcg ttt cag tcc gtg gtc tgg ggt ctg acg gtg ggg 152
 Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr Val Gly
 50 55 60

	tcg tgg ata ggt tog tgg ggg ggt ctg atg gtg ggg ggg gcc tgg ccg	240
	Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ala Ser Pro	
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5	tat gtc ggc tgg atg agc gtc acc ggg ggg cag gcc gag ctg acc gcc	288
	Tyr Val Ala Trp Met Ser Val Thr Ala Gly Glu Ala Glu Leu Thr Ala	
	88 90 95	
10	gcc cag gtc cgg gtt ggt ggg ggg gcc tac gag aag ggg tat ggg ctg	336
	Ala Glu Val Arg Val Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu	
	100 105 110	
15	aag gtc ccc ccg ccg gtc atc gcc gag aac cgt gct gaa ctg atg att	384
	Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile	
	115 120 125	
20	ctg ata ggc acc aac ctg ttg ggg caa aac acc ccg ggg atc ggg gtc	432
	Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val	
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	aac gag gcc gaa tac ggc gag aag tgg gcc caa gac gcc gcc ggg atg	480
	Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Glu Asp Ala Ala Ala Met	
	145 150 155 160	
25	att ggc tac gcc gag ggg aag ggg aag ggg aag ggg aag ttg ctg ccg	528
	Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro	
	165 170 175	
30	ctc gag gag ggc ccg gag atg aac agc ggc ggt ggg ctg ctg gag ccg	576
	Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln	
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35	gcc gcc ggc gtc gag gag gcc tcc gac acc gcc ggg gag aac cag ttg	624
	Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Glu Leu	
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40	atg aac aat gtc ccc cag ggg ctg caa cag ctg gcc cag ccc aag cag	672
	Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln Pro Thr Gln	
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	ggc acc aag cct cct tcc aag ctg ggt ggc ctg tgg aag aag gtc tgg	720
	Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser	
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	Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His	
	245 250 255	
50	atg tog atg acc aac tog ggt gtg tog atg acc aac aac ttg agc tog	816
	Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser	
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55	atg ttg aag ggc ttc gct ccg ggg ggg gcc gcc cag gcc gtc caa acc	864
	Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Glu Ala Val Gln Thr	
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60	ggg ggg caa aac ggg gtc cgg ggg atg agc tog ctg ggg agc tog ctg	912
	Ala Ala Glu Asn Gly Val Arg Ala Met Ser Ser Ser Leu Gly Ser Ser Leu	
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	ggt tct tog ggt ctg ggc ggt ggg gtg gcc gcc aac ttg ggt cgg ggg	960
	Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala	
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65	gcc tog gtc ggt tog ttg tgg gtg ccg cag gcc tgg gcc ggg gcc aac	1008
	Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala Ala Ala Asn	
	325 330 335	

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	Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr	
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5	agc gcc gcg gaa aga ggg ccc ggg cag atg ctg ggc ggg ctg ccg gtg	1134
	Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu Pro Val	
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	Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly Val Leu Arg	
	370 375 380	
15	gtt cag cag cga ccc tat gtg atg cag cat tcc cag gca gcc ggc gat	1230
	Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala Gly Asp	
	385 390 395 400	
20	atc gcc cag cag gcc ttg tgg cag gac cgg ttc gcc gac ttc ccc gcg	1248
	Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala	
	405 410 415	
	ctg ccc ctg gac ccg tcc gcg atg gtc gcc caa gtg ggg ccc cag gtg	1296
	Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val	
	420 425 430	
25	gtc aac atc aac acc aaa ctg ggc tac aac aac gcc gtg ggc gcc ggg	1344
	Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly	
	435 440 445	
30	acc ggc atc gtc atc gat ccc aac ggt gtc gtc ctg acc aac aac ccc	1392
	Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His	
	450 455 460	
35	gtg aac gcg ggc gcc acc gac atc aat gcg ttc agc gtc ggc tcc ggc	1440
	Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly	
	465 470 475 480	
40	caa acc tac ggc gtc gat gtg gtc ggg tat gac cgc acc cag gat gtc	1488
	Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val	
	485 490 495	
	gcg gtg ctg cag ctg cgc ggt gcc ggt ggc ctg cag tgg gcg gcg atc	1536
	Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile	
	500 505 510	
45	ggt ggc ggc gtc gcg gtt ggt gag ccc gcc gtc gcg atg ggc aac agc	1584
	Gly Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser	
	515 520 525	
50	ggt ggg cag ggc gga aag ccc cgt gcg gtg cct ggc agc gtg gtc gcg	1632
	Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala	
	530 535 540	
55	ctc ggc caa acc gtg cag gcg tgg gat tgg ctg acc ggt gcc gaa gag	1680
	Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Gln	
	545 550 555 560	
60	aca tgg aac ggg ttg atc cag ttc gat gcc gcg atc cag ccc ggt gat	1728
	Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp	
	565 570 575	
	tgg ggc ggg ccc gtc gtc aac ggc cta gga cag gtg gtc ggt atg aac	1776
	Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn	
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<210> SEQ ID NO:20
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 <223> Description of Artificial Sequence:bi-fusion
 protein Tbm9-Kals (designated Mtb89F)

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 20 25 30
 15 Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp Leu Phe
 35 40 45
 Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr Val Gly
 50 55 60
 20 Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ala Ser Pro
 65 70 75 80
 25 Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala
 85 90 95
 Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu
 100 105 110
 30 Thr Val Pro Pro Pro Val Ile Ala Gln Asn Arg Ala Glu Leu Met Ile
 115 120 125
 Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val
 130 135 140
 35 Asn Glu Ala Gln Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met
 145 150 155 160
 40 Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro
 165 170 175
 Phe Gln Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln
 180 185 190
 45 Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu
 195 200 205
 Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln Pro Thr Gln
 210 215 220
 50 Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser
 225 230 235 240
 Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His
 245 250 255
 55 Met Ser Met Tyr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser
 260 265 270
 60 Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Glu Ala Val Gln Thr
 275 280 285
 Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu
 290 295 300
 65 Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala
 305 310 315 320
 Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala Ala Ala Asn

325 330 335
 Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr
 340 345 350
 5 Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu Pro Val
 355 360 365
 10 Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly Val Leu Arg
 370 375 380
 Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala Gly Asp
 385 390 395 400
 15 Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala
 405 410 415
 Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val
 420 425 430
 20 Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly
 435 440 445
 Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His
 450 455 460
 Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly
 465 470 475 480
 30 Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val
 485 490 495
 Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile
 500 505 510
 35 Gly Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser
 515 520 525
 Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala
 530 535 540
 Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Gln
 545 550 555 560
 45 Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp
 565 570 575
 Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn
 580 585 590
 50 Thr Ala Ala Ser
 595

55 (2) INFORMATION FOR SEQ ID NO:21: DPV (MTB8.4)

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 500 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

65 CCGTGCATG TCGTTGACCG TCGGCGCCGG GGTGCGCTCC GCAGATCCCG TGGACCGGGT 50
 CATTAACACC ACCTGCAATT ACGGCGAGGT AGTAGCTTCG CTCACGCGCA CGGATCCGGG 100
 GCGTGGCGCA CAGTTCAACG GGTACCGGGT GCGGCACTCC TATTTGCGCA ATTCTCTCC 150
 CGCAGCGCCA CTCAGGCGCG CTCGCATGCG GCGGCAATTG CAGGCTGTGC CGGGGGCGGC 200

ACAGTACATC GGCCTTGTCT AGTCGGGTGC CGGCTCTTGC AACAACTATT AAGCCCATGC 300
 GGGCCCATTC CCACGACTCC GATCTCTTGC CGGGCTAGG CCAGATTGCC CCGCTCTCTA 360
 ACGGGGCCCA TCCCHCCACC CGGCATCTTC GCGGGGGCTA GGCAGATTG CCCCCTCTT 420
 CAACGGGCCC CATCTCTTGC CGAATTCTTG CAGCCCGGGG GATCCACTAG TTCTAGAGCC 480
 GCGCCACCCG CGGTGGAGCT 500

(2) INFORMATION FOR SEQ ID NO:22: DPV (MTB8.4)

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 96 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Val Ala Met Ser Leu Thr Val Gly Ala Gly Val Ala Ser Ala Asp Pro
 1 5 10 15
 Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val Val Ala
 20 25 30
 Ala Leu Asn Ala Thr Asp Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser
 35 40 45
 Pro Val Ala Gln Ser Tyr Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro
 25 50 55 60
 Gln Arg Ala Ala Met Ala Ala Gln Leu Gln Ala Val Pro Gly Ala Ala
 65 70 75 80
 Gln Tyr Ile Gly Leu Val Gln Ser Val Ala Gly Ser Cys Asn Asn Tyr
 85 90 95

(2) INFORMATION FOR SEQ ID NO:23: MSI (MTB9.8)

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 585 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TGGATTCCGA TAGCGTTTC GCGCCCTCGA CGGCGACCA CGGCGCGCG GCTTCCBAAC 60
 GGGGGGCCGG GAGCTTGGGA TTCCCGGGGA CGGCAACCA AGAACGCCG GTCCGGGGGG 120
 TCGGCTGAC CGCCTGCGC GTTGATGAGT TCGGCAAGG CCGTCGATG CGATGCTGC 180
 CGGCGACTG GAGCGGGGC ASCACGAGC CCGAGCGGC CGACGATCG GCGAGGGGG 240
 GAGGCGACG CTTACCGCAC GACAGCAAGT AACCGATTG CGATCAGGT GACCCGTAC 300
 GGTTCGAAAG GAGAGATGTT ATGAGCTTT TGGATGCTA TATCCACAG TTGCTGGCT 360
 CCCAGTGGC GTTTCGGCC AAGGCGGGC TGATGCGCA CACGATCGT CAGGCGAGC 420
 AAGCGGCGAT GTGCTCTCG GCTTTTACC AGGCGAGTC GTGCGCGGG TTTCAGGCTG 480
 CCGATGGCCG GTTGTGGCG GCGGCCGCC AAGTCAACG CTGTTGGAT GTGCGCAGG 540
 CGATCTGGG TGAGTCCGC GTTACTATG TGGCGCGCA TGGT 585

(2) INFORMATION FOR SEQ ID NO:24: MSI (MTB9.8)

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 97 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser
 1 5 10 15
 5 Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala
 20 25 30
 Gln Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Gln Ser Ser
 35 40 45
 10 Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys
 50 55 60
 Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Gln Ala Ala
 65 70 75 80
 Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ser Thr Tyr Thr Gly
 85 90 95
 15 Phe

(2) INFORMATION FOR SEQ ID NO:25: MTX (MTB9.9A)

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1742 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CGGCTCTCTT TCAAGCTGCT AAGTTCGGTG GGCAGTCCG CCGCGGCTGC ATATGCGACC 60
 AATAAGCTCT GTCCATGGA TACCGGACG GCAAGACCT AGAGCGGATC AGCGGAGCCG 120
 35 GTCCGGAACA CTACCGCTC CACCTCAGC CCTGCGCCT TCGCGAGAT CGAGCCGAGG
 TTCTCATGGT CGTTAAGGCT TTCCAGACT GCGACGCTGC CGCGCCCGGC CACCACCTGA 240
 GCAAGCTCTG GCTCCGGCAC CCGCGCGCG GCTGCCAACA CCCCAGGATY GAGATGGAG 300
 CCGATCAGCC GTCCATGAC ATGAGCGAC GCTCGATAGT ACGGCTGCTC GACACCGCTC 360
 AGATCATCTT TTAGTTCGG CAGCGCGCG TCGGTTCGCA ACAGCGCCAG CGGCTGAGC 420
 40 CTTGAGGCCA GCATCGCTG CACCACGAG ACACCTTCGG CAGTACCAA CGCCTTGCC 480
 GTCCGCGGAT CGGCGGCGC GTCGATGCT TTCAAGTCA GGAATCTCT GAGCGCTGG 540
 TCGTGGGAT CCGAGAGCT CTAACATCG AGGCTCTCG GGTCTCTGCG ACAACGCGCT 600
 TCGTTACCG GCTTCTCTG ACCAGAGCA GCATCAGAT GCGCGCGCTG CCGAGGATGT 660
 CAGCTCTGCT CGGCTTCAG GTCCGAGCC GCTGAGCCAG CCACTCTTGC AGAGAGCGCT 720
 45 TGCTGCGATT AATCGGAGA GAGAGACAG ATGCTGCTG TGACCAACA GCGGAGAGCC 780
 CTGCGAGCTG CCGCGCGGAA CTTACAGGCT ATTGCGGCA CAATGAGCG CCGAGACCG 840
 GCGCGGCTG CTTCAACCC CCGAGTATG CCGCGAGCC CCGATGAGT ATCAGGCTG 900
 ACCGCGCTC AGTTCTCTG GCAAGCGCG ATGTCGAAA CCGTCAAGCG CCGAGCGCG 960
 GCGATTCAG AATGTTCTG GAGACGCTG GTGCGAGCT CTGCTCATA CGCGCGGACC 1020
 50 GAGCGGCGCA ACGCAGCGC TGCGGCTGA AGCGCTCGC AGGAGCTTC TGAAGGAGAG 1080
 GCGGAGATC CCGAGTCTC GGTTCAGCG TTGCGCCAG CCGCAGCGCA TTCAATATC 1140
 GCGCTCATA ACAGCAGAG ATCTAGGCT TCACTACTAA GAGACAGGC AACATGCGCT 1200
 CAGCTTTTAT GACGATCCG CAGCGGATG GGGACATGC GCGCGCTTTT GAGGTGACG 1260
 CCGAGAGCT GAGGAGCGG GCTCGCGCG TGTGCGCTC CCGCAAAAC ATTTGCGGT 1320
 55 CCGCTCGAG TCGCATHGC GAGCGAGCT GCGTACAGC CAGGAGCTAG ATGATCAGG 1380
 CGTTTCGCA CATCTGAGC ATGCTGAGC GGTGCGTGA CCGGCTGCTT CCGAGCGCCA 1440
 ACAGTACGA ACAGCAAGAG CAGGCTTCC AGCAGATCT GAGCAGTAT CCGCGAAGC 1500
 CAGAGCTTGG TACGTTTCT CAGCTTAGG GAGCAGCAAT ATGAGGATTA ATTACCGTT 1560
 CCGGAGCTC GAGCTCATG GCGCATGAT CCGGCTCAG CCGGCTTGC TTGAGGCGA 1620
 60 GCGTCAAGCC ATGCTCTCT ATGCTTTCG CCGGCTGAC TTTTGGGCG CCGCGCTTC 1680
 GGTGCTTGC CAGGATTTCA TTACCGGTT GCGCGCTAAC TTCCAGGTGA TCTACAGCA 1740
 GZ 1742

(2) INFORMATION FOR SEQ ID NO:26: MTI (MTB9.9A)

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2836 base pairs

(S) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

GTGATTCG  TTCCGCGGCG  CCGCAAGAC  CACCAACTCC  GCTGGGGTGG  TCGCACAGGC  40
GGTTGCGTCG  CTCAGCTGAC  CCAATCCCAA  TGAATGGTGG  CTGAGTTCGG  TTCTGGGCT  120
CGATTACCCC  CACGGAAGAG  ACGACGATCG  TTCTTTTGGT  CGTTCAATCG  TACTTGGCGA  180
CGGCGATGCG  GCGGTTTCCT  ACGTCGATCG  CACAGCAGCT  GAGCTTCGGC  CCAGGGGGCA  240
CAACGGGTGG  CTCGCGCGGA  GCTGGGTACC  CAACGCGACA  ATTGCGCGGC  CTGGGTGCGG  300
GCGCGGGGCT  GTCGCGGAGT  TTGCGCGCGG  CCGAGCGGGT  CGGAGGTTGG  TCGGTGCCGC  360
CAAGTTGGCG  CGTCGCGGCT  CCGGCTTTCG  CCGAGAGAGC  TGAAGCGGGC  ACGCGGATGT  420
CGCTCATCGG  CCAAGCGTCC  AGCTGCGGTC  AGGAGGCGCT  GCTTCGAGCG  ATACCGCTGG  480
CAGAGCGTGG  GCGCGGTACA  GCGCGCTTCG  CTGACCGATA  CGGTTTCGGC  CACAGCGTGA  540
TTACCGCGTC  TCGTTCGGCG  GATAGCTTT  CCACTCGGTC  TCGCGGGGCG  CCGGAAATGT  600
TGCAGATGAG  GATCGACCGC  GCGGTTGGGT  AAGCGCGCGA  CAGCGGACTA  TCAATGCGCA  660
CGCGGGGGCT  TGAAGCGCAA  TTGACGTTTC  CGAGCGGGCT  TTATCTCGCG  CAGGATTTCA  720
TCCCGAGCGC  GGTTCGTTGG  CCGATAAATA  CGTTCGTCAG  CGCGACTGCT  CCGGCTGAAT  780
TGGATGCTCT  GCGCGCGCGC  TCGACGCGCA  GTATCTCGAG  TGGCGCGCAA  ACCCGGTCAA  840
AGCGTGTGAC  TGTGGCGGTA  CCGAGGTGTA  ATTGCGGTG  CCACTGCTG  AAGCTTGGC  900
AAGCGGTGCG  ATCGAATGCA  ACTTGTTCG  TCGAGTGTAT  CTACTCTCTT  GCGAGAGAGC  960
GTTCTGTGGA  TTAATGGAAG  GAGGAGAGCA  GCGTTCGTT  CGTACCGACA  CAGCGGAGAG  1020
GCTGGCGAGC  TCGCGCGCGC  AAGCTACGCG  GTATTGCGAC  GAGCAATGAG  GCGCAGAGCG  1080
CGGCGCGCGC  TCGTTCAGCT  ACCGAGGTAG  TCGCGCGAGC  CGCGATGAG  GTATCAGGCG  1140
TACCGCGCGC  TCACTTTCCT  GCGACCGCGC  AGATGTACCA  AAGCTTCAGC  GCGCAGCGCG  1200
CGGCGCTTCA  CGAATGTGTC  GTGACAGCGC  TCGTTCGCGC  TTCTGCGTCA  TACCGCGCGC  1260
CGGAGCGCGC  CAGCGCGAGC  GCTGCGGCGT  GAGCGGCTTC  GCGGAGAGCT  GCTGAGAGAG  1320
AGCGGAGAGC  TCGGAGGTC  TCGGTCAGCG  GGTTCGCGCG  GCGCGCGCGC  GGTTCAGCTA  1380
TGGCGCTTCA  TACAGCGAGA  CGATCTAGCG  ATTCACTACT  AAGGAGAGAG  GCAACATGCG  1440
CTCAGCTTTC  ATGAGCGATC  CGCATGCGAT  GCGGAGAGT  GCGCGCGCGT  TTAGGTTGCA  1500
CGCGCGAGCG  GTGAGGAGCG  AGCTTCGCGC  GATGTGGGCG  TCGCGCGCAA  AATTTTCGCG  1560
TGGCGGCGCG  AGTTCGAGCG  CCGAGCGGAG  CTGCTAGAGC  ACCGTGAGCT  AGATGAGTCA  1620
GCGCTTTCG  AAGATCGTGA  AATTCGCTCA  CGGCGTGGGT  GAGCGGCTTC  TTGCGGAGCG  1680
CAACAAGTAC  GAGACGAGAG  AGCAGCGCTC  CGAGCAGATC  CTGAGCAGCT  AGCGCGGAAA  1740
GCGACAGCTG  CTTACGCTTC  CTCACATGAG  GAGACAGCA  ATATGAGGAT  TAAATACGAG  1800
TTGCGGAGCG  TCGAGCTTCA  TCGCGCGCTG  ATCGCGGCTC  AGCGCGGCTC  GCTTGAAGCG  1860
GAGCATGAGG  CGATCGTTCG  TGAATGTGTC  GCGCGGCGTG  ACTTTTGGCG  CGGCGCGCGT  1920
TGGGTGCTTC  GCGAGGAGTT  GATTCAGGAG  TTGCGCGGTA  ACTTCAGGTT  GATCTACGAG  1980
CAGCGCGAGG  CCGACGCGCA  GAGGTCGAG  GTGCGCGGCA  ACAACATGCG  GCAACCGGAG  2040
AGCGCGGTCG  GCTCAGCTTC  GCGCTAAAGC  TGAATTCAG  TCGCGCGAGC  ACACCAAGCA  2100
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CAGCAGGTA  CCGGAGCGCA  CATGAGCTTC  AAGCTCAGCG  GCTTCTGAGT  GCTTCAGGCG  2220
CTACTGAGTA  TCGCGGAGTT  TCGCGCTGAG  TTACTTTCCT  GCGGCTAGCT  CTCTACCGAT  2280
TCCATGAGCT  GGTAAAGCA  GCGCGCGGCG  ATGCGCGCTC  TCGCGGAGCA  GCGGCTTTCG  2340
GTCAAGAGCG  CGGTCAAGCA  ACAGGTGCTC  GCGCGGATGA  AGGTGCTTGC  CGCAGCTGAT  2400
CTTGAAGTGG  TCGCGCTGCT  GTCAAGCGCG  AAGTTGCTGT  ACGCGGTCAT  AGAGGAGGAG  2460
AAGCGCGCGC  CGGTTTCGCG  TGAATTCCT  GAGCAATGAG  TCGCGGTTGT  GTTGGCGCGG  2520
CGAGCGGAGC  ACTGCGTTC  GCGGTTAGCG  GTTGCAGATG  ACATCAGGCT  GATGAGCTG  2580
AGCGTTCGCG  ATAGCGCTTC  GATCGCGGCA  CTGCTAATG  ACGCTCTGGA  GTCGATTGAC  2640
CAGCGCGAGC  CAGCGCGGAT  CAACGCGTTC  AAGTTCGCA  TGAAGGAGAT  CTGCTGCGGA  2700
ATTGCGCGCG  AGCGAGGAG  CGGTGCTGCT  GAGCAGGCGA  TCGATCAGTA  TCACTGAGCG  2760
GCGCGGATCC  TTGGCGATCT  GGTGAGGAG  GAGCGCGGCG  CGCGGAGAGC  TCTGCGAGAT  2820
CGATGCGTTC  TTCCCG

```

(2) INFORMATION FOR SEQ ID NO:27: MTI (NTS9.5A)

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
1 5 10 15
Ile Arg Ala Leu Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile
20 25 30
Ser Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala
35 40 45
Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
50 55 60
Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
65 70 75 80
Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
85 90

(2) INFORMATION FOR SEQ ID NO:28: HTCC#1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1200 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CAGGCTATGAG CAGAGCGCTTC ATCATCGATC CAACGATCAG TGCGATTGAC GGCTTGTAAG 60
ACCTTCCTGGG GATTGGAATA CCGAACCAGG GGGGTATCTT TTAAGCTCTA CTAGAGTACT 120
TCGAAAAAGC CCTGGAAGAG CTGGCAGCAG CTTTTCGGG TGAATGCTAG TTAGGTTCGG 180
CGCGGACAGA ATACGCGGCT AAAAACCGCA ACCCGGTGAA TTTTTCAG GAACTGGCAG 240
ACCTGATGTC TCAGCTCATC AGCTGATCC ACAGCCAGGC CAACGCTGC CAGACGACCC 300
GGGACATCTT GAGGGGCGCT AAAAAGGTC TCGAGTTCTT GCGCCCGGTG GCTGTGGACC 360
TGACCTACAT CCGGCTGCTC GGGCAGCGCC TATCGGCGC CTTCGAGGGG CCCTTTTTCG 420
CGGGCGGATG GGCCTAGTG GCGGCGGCGC TTGCTACTT GGTCTGAAA ACCTGATCA 480
ACCGGACTCA ACTCTTCAA TTCTTTGCCA AATTGCGGAA GTTGCTGCG GCGGCGATG 540
CGGACATCAT TTGGATGTC GCGGACATCA TCAGGGGCAC CCTCGAGAG GTGTGGAGT 600
TCATCAGAAA CCGCTCAAC GGCCTGAAA AGCTTTGGGA CAAGCTCAG GGTGCTGTA 660
CGGACTCTT CTCTGAGGG TGGTCAAGC TGAATCTCTT CTTTGGGGC GTCCCGGCT 720
TGACCGGCGC GACGAGCGC TTGTGCAAG TGACTGCTT GTTCTGTCG GCGGTCTGT 780
CGGATCTCT GGGCTTGGCT CAGCGGATA GCTTGGGAG CTCAGCCAGC TTGCGCGCC 840
TGCGGCGAT TGGGGCGCG TCGGTTTTC GGGCTTTCG GAGGCTGCT CAGGTCCAT 900
CGGCTTCAAC TCGGAGGCG CTAGCGGCC GAGCTGATG CCGGTCGCG CCGCTGCGG 960
AGCGGTCGG CCGGCACTG CAGCTGCTT CCGGCGAGG TTCCCAAGT ATGCGCGAG 1020
CGTGGGCAAT GGGCGGCAAT CAGGCTCTT CCGGCGGCTC GAAAGCGAG ACHAGCAAG 1080
AGTACTCGA AGGCGCGCG CCGGCACTG AAGGCGCGA GCGCGCGCA GTTCAAGCTG 1140
ACGCGGCGG TGGCAAAAG GTCTGCTAC GAAAGCTCTT CTAAAGGCT GCGGAGCCAA 1200

(2) INFORMATION FOR SEQ ID NO:29: HTCC#1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 392 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
 1 5 10 15
 Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
 20 25 30
 5 Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
 35 40 45
 Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
 50 55 60
 10 Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
 65 70 75 80
 Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
 85 90 95
 Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val
 100 105 110
 15 Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
 115 120 125
 Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
 130 135 140
 20 Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
 145 150 155 160
 Thr Glu Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
 165 170 175
 Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Thr
 180 185 190
 25 Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
 195 200 205
 Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
 210 215 220
 30 Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
 225 230 235 240
 Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
 245 250 255
 Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
 260 265 270
 35 Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
 275 280 285
 Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
 290 295 300
 40 Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
 305 310 315 320
 Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
 325 330 335
 Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
 340 345 350
 45 Lys Gly Thr Thr Thr Lys Lys Tyr Ser Gln Gly Ala Ala Ala Gly Thr
 355 360 365
 Glu Asp Ala Glu Arg Ala Pro Val Gln Ala Asp Ala Gly Gly Gly Gln
 370 375 380
 50 Lys Val Leu Val Arg Asn Val Val
 385 390

(2) INFORMATION FOR SEQ ID NO:30: MTOC#2

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1441 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

60

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

65 GAGGTTCTCTG GCAATGAAAT TGGGCTTTT ACCTCGGAA GTCAATTCAG GCCGAATGTA 60
 TTCGGGPDG GGGCCGAAAT CGATGTTAG CGCGCGGCG CCCTGGGAGG GTGTGGCCGC 120
 GCGGTTGACT TCCCGCCCGG TCTCGTATGG ATCGGTGGTG TCGACGCTGA TCGTTGAGCC 180
 GGGATGAGG CCGCGCGCGG CCGGATGCG GCGCGCGCA ACCCGTATG TGGGTGCT 240

	GGCCGCCAGG	GCAGCCCTGG	CGAAGGAGAC	GGCCACACAG	GGCAGGSCAG	CGCCGGAAGC	300
	GTTCGGGAGG	GGTTTCGCGA	TGACGGTGGC	ACCCCTCCTC	GTCCGGGSCA	ACCCGAGCGG	350
	GTTCGATGTG	CTGGTCGGCG	CGACATTCCT	GGGGCAAAAC	AGTCCGGGCA	TCCCGGCTAC	400
5	CCCGGCCGAG	TATGCCGAAA	TGTGGGCCCC	AGACCTCTCC	GTATATGTAC	GCTATGAGGG	450
	GGCATCTGCG	GGCGGCTCGG	CGTTGCGCGC	GTTCACCTCA	CCCGTGCAGG	GCACCGGCGC	500
	GGCCGGGCGC	GGCGGCGCGG	CGCGGGGCGC	CCAGSCCGCC	GGTCCGSCCG	CCGTTGCGGA	550
	TGCACAGGGG	ACACTGGGCG	AGCTGGCGCG	GGGATCTCTG	AGGACACTTC	TGTCCGCAAT	600
	GGCCGCCAAG	GCTGATCCGC	TGACATCGGG	ACTGTTGGGG	ATCCGCTCGA	CCCTCAACCC	650
	GCAGATGAGA	TCCGCTGAGC	CGATATGGAT	CCCTACCGCG	ATAGGGGAAT	TGGACGTGAT	700
10	CGCGCTCTAC	ATTGCATCCA	TGCGGACCGG	CAGCAATGCG	CTCGCATCCA	CGACACGGCG	750
	CAGACCTCTG	CACATCGGCG	TATACGGGAA	CGCGGGCGGG	CTGGGACCGA	CGCAGGGGCA	800
	TCCACTGAGT	TCCGGGACCG	AGGAGCGCGA	GGCGCACTGG	GGCCCTCTCG	GGGCGCGCGC	850
	GGCGGCTGTC	GGCGGCTGTC	GGCAGCGAGC	ATGATGCGGA	GGCTTGTGCG	TGCGCGCAGC	900
	CTGGACCAAG	GGCGGCTGCG	AGATCCAGCT	CGCGTTGCGG	GGCAGACCGA	CTTCAGCTTC	950
15	CAGCGCGCGG	CGCGACCGCA	CGCCCTTAAA	CGCGATGCGG	CGAGGCTCTG	TGACCGGGAT	1000
	GGCTTTGGCG	AGCCTGGCGG	CACCGCGGAC	GACCGGGGGT	GGCGGCACCC	GTACCGGCGC	1050
	CAGCACTGAC	GGCCAGAGAG	AGCGCGCGAA	AGCCCGCGTA	GTGTGATTA	GAGAGCAGCC	1100
	GGCGGCGCGA	AACCGCGCGC	GGTAAAGCTC	CGKACCGCT	TCTTCGCTCG	GGGAAAGATG	1150
	CGTCTGAGC	GTGCTATCTC	GGCGGCGCGT	TGACACCGCT	TGTGATGCGG	TACGGCTATG	1200
20	GACGACGCTG	TCTGAGCTTC	CGCGGCGCTAT	CAGACCGATT	TGCTGCGCAA	CGTCAGCGAA	1250
	G						1441

(2) INFORMATION FOR SEQ ID NO:31: MTC282

25

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 423 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

35

	Met	Asp	Phe	Gly	Leu	Leu	Pro	Pro	Glu	Val	Asn	Ser	Ser	Arg	Met	Tyr
	1			5					10					15		
	Ser	Gly	Pro	Gly	Pro	Glu	Ser	Met	Leu	Ala	Ala	Ala	Ala	Ala	Trp	Asp
				20					25					30		
40	Gly	Val	Ala	Ala	Glu	Leu	Thr	Ser	Ala	Ala	Val	Ser	Tyr	Gly	Ser	Val
				35					40					45		
	Val	Ser	Thr	Leu	Ile	Val	Glu	Pro	Trp	Met	Gly	Pro	Ala	Ala	Ala	Ala
				50					55					60		
	Met	Ala	Ala	Ala	Ala	Thr	Pro	Tyr	Val	Gly	Trp	Leu	Ala	Ala	Thr	Ala
45									70					75		
	Ala	Leu	Ala	Lys	Glu	Thr	Ala	Thr	Gln	Ala	Arg	Ala	Ala	Ala	Glu	Ala
				85					90					95		
	Phe	Gly	Thr	Ala	Phe	Ala	Met	Thr	Val	Pro	Pro	Ser	Leu	Val	Ala	Ala
				100					105					110		
50	Asn	Arg	Ser	Arg	Leu	Met	Ser	Leu	Val	Ala	Ala	Asn	Ile	Leu	Gly	Gln
				115					120					125		
	Asn	Ser	Ala	Ala	Ile	Ala	Ala	Thr	Gln	Ala	Glu	Tyr	Ala	Glu	Met	Trp
				130					135					140		
	Ala	Gln	Asp	Ala	Ala	Val	Met	Tyr	Ser	Tyr	Gln	Gly	Ala	Ser	Ala	Ala
55				145					150					155		
	Ala	Ser	Ala	Leu	Pro	Phe	Thr	Pro	Pro	Val	Glu	Gly	Thr	Gly	Pro	
				160					165					170		
	Ala	Gly	Pro	Ala	Ala	Ala	Ala	Ala	Ala	Thr	Gln	Ala	Ala	Gly	Ala	Gly
				180					185					190		
60	Ala	Val	Ala	Asp	Ala	Gln	Ala	Thr	Leu	Ala	Gln	Leu	Pro	Pro	Gly	Ile
				195					200					205		
	Leu	Ser	Asp	Ile	Leu	Ser	Ala	Leu	Ala	Ala	Asn	Ala	Asp	Pro	Leu	Thr
				210					215					220		
	Ser	Gly	Leu	Leu	Gly	Ile	Ala	Ser	Thr	Leu	Asn	Pro	Gln	Val	Gly	Ser
65				225					230					235		
	Ala	Gln	Pro	Ile	Val	Ile	Pro	Thr	Pro	Ile	Gly	Glu	Leu	Asp	Val	Ile
				240					245					250		
	Ala	Leu	Tyr	Ile	Ala	Ser	Ile	Ala	Thr	Gly	Ser	Ile	Ala	Leu	Ala	Ile

```

                260                265                270
Thr Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly
275                280                285
5 Gly Leu Gly Pro Thr Glu Gly His Pro Leu Ser Ser Ala Thr Asp Glu
390                395                400
Pro Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala
305                310                315                320
Gly Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser
325                330                335
10 Trp Thr Thr Ala Ala Pro Gln Ile Gln Leu Ala Val Gln Ala Thr Pro
340                345                350
Thr Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met
355                360                365
15 Pro Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg
370                375                380
Gly Thr Thr Gly Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly
385                390                395                400
Gln Gln Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Gln Gln Pro
405                410                415
20 Pro Pro Gly Asn Pro Pro Arg
420

```

(2) INFORMATION FOR SEQ ID NO:32: ESAT-5

25

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
30 (D) TOPOLOGY: linear

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

35 ATTACGAGAC AGCAATGANA TTTCGGGGGT ATCGAGGCGC CGGCAAGGCG AATCCAGGGA      60
AATGTCAAGT CATTTCATC CTCCTTGAC GAGGGGAGAC AGTCCCTGAC CAGCTCGCA      120
GGGCTGGG GCGGTAGCG TTGGAAGCG TACC                                154

```

(2) INFORMATION FOR SEQ ID NO:33: ESAT-5

40

```

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
45 (D) TOPOLOGY: linear

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```

50 Met Thr Glu Gln Gln Trp Asn Phe Ala Gly Ile Gln Ala Ala Ala Ser
1 5 10 15
Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly
20 25 30
Lys Gln Ser Leu Thr Lys Leu Ala Ala Ala Trp Gly Gly Ser Gly Ser
35 40 45
55 Glu Ala Tyr
50

```

(2) INFORMATION FOR SEQ ID NO:34: Tb38-1

60

```

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 337 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
65 (D) TOPOLOGY: linear

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

5 CGGCACGAGA GACCGATGCC GCTACCCCTCG CCGACGAGGC AGGTAAATTC GAGCGGATCT 60
 CCGCGGACCT GAAAACCCAG ATCGACGAGG TCGAGTCGAC GGCAGGTTCC TCGCAGGCCC 120
 AGTGGCGGGG CGCGCGGGGG ACGGCCGCCG AGCGCGCGGT GGTGCGCTTC CAGCAAGCAG 180
 CCAATAAGCA GAAGCAGGAA CTCGACGAGA TCTCGACGAA TATTCGTCAG GCGCGCGTCC 240
 ANTACTCGAG GCGCGACGAG GAGCAGCAGC AGCGCTGTC CTCGCAATG GCGTCTGAC 300
 CCGCTAATAC GAAAGCAAC GAGGCA 327

(2) INFORMATION FOR SEQ ID NO:35; Tb39-1

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile
 1 5 10 15
 Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly
 20 25 30
 Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala
 35 40 45
 Ala Val Val Arg Phe Gln Gln Ala Ala Asn Lys Gln Lys Gln Glu Leu
 50 55 60
 Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg
 65 70 75 80
 Ala Asp Glu Glu Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
 85 90 95

(2) INFORMATION FOR SEQ ID NO:36; Tb2a3

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 542 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GAATTCGGCA CGGAGGGTGA TCGACATCAT CCGGACTAGC CCCACATCCT GCGAACAGGC 60
 GCGCGCGGAG CGCGTCCAGC GCGCGCGGGA TAGCGTCGAT GACATCCGCG TCGCTCGGGT 120
 CATTGAGCAG GACATGGCCC TCGACAGGCG CCGCAAGATC AACTACGCGA TCAAGCTCGA 180
 AGTGTGCTTC AAGATGAGGC CCGCGCAACC CGCTAGCAC GCGCGCGGGA GCAAGACGCA 240
 AATGCGACG GTTTCGGTT GATTGTTGCG ATTTGTTGTC TGCTCGCGGA GCGCTACGAG 300
 GCGCGCGCCA GGTCCGCGTG CTGCGGTATC CAGGCGTACA TCGCGATTCC GCGCGCCAGC 360
 CCGGATTAAT TCTTTCGCT CCGCCGAAAC TCGCGATCC CCGCGGAGC TCGTGTATGA 420
 CGGTGCGCAG CGGTGCGATG CCGGATTCG CCGAGGAAAC GTGCTGCCAG GCGGTAGGA 480
 AGGTTCCTTA GCGCGCGTGT CTGACCGCT CTGCTGCGCG CCGTCTGTC GCGAGCGAGC 540
 G3 542

(2) INFORMATION FOR SEQ ID NO:37; Tb2a3

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Val Ile Asp Ile Ile Gly Thr Ser Pro Thr Ser Trp Glu Gln Ala Ala
 1 5 10 15
 Ala Glu Ala Val Gln Arg Ala Arg Asp Ser Val Asp Asp Ile Arg Val
 20 25 30

Ala Arg Val Ile Glu Gln Asp Met Ala Val Asp Ser Ala Gly Lys Ile
 35 40 45
 Thr Tyr Arg Ile Lys Leu Glu Val Ser Phe Lys Met Arg Pro Ala Gln
 50 55 60
 5 Pro Arg
 65

(2) INFORMATION FOR SEQ ID NO:38: 38 kb

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1993 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

20 TGTTCTTCTGA CGGCACGCTG GTGGAGGAAG GGGCCACCGA ACAGCTGTTT TCCTCGCCGA 60
 ABCATGCGGA AACCGCCCGA TACGTGCGCG GACTGTGCGG GCACGTCAAG GACGCCAAGC 120
 GCGGAAATTG AAGAGCACAG AAGGTATGCG CGTGAAATTT GTTTGCATA CGCTGTTGGC 180
 25 CGTGTTCACC GCTGCGCCGC TKTGCTAGC AGCGGCGGCG TGTGCTCGA AACCAACGAG 240
 CGTTCGCTT GAAACGCGCG CGGCGCGCGG TACTGTGCGC ACTACCCCGG GTTCGTGCGC 300
 GTTGACGTTG GCGGAGACCG GTAGCAGCTT GCTCTACCGG CTGTTCAAGC TGTGGGCTCC 360
 30 GGCCTTTCAC CAGAGGTATC CAAACGTCAC GATCAAGCTT CAGGSCACCG GTTCGTGCTC 420
 CGGATTCGCG CAGGCGCGCG CGGAGACGCT CAACATTCGG GCTTCGACCG CCTATCTGTC 480
 35 GGAAGGTGAT ATGCGCCCGC ACAAGGCGCT GATGAACATC GCGCTAGCCA TGTCCGCTCA 540
 GCAGGTCAAC TACAACCTGC CTGAGTTCAG CAGGACCTTC AAGCTGAACG GAAAAGTCTT 600
 GCGGCGCGTG TACGAGGCGA CCATCBAAC CTGGAGACAG CCGCAGATCG CTGCGCTCAA 660
 40 CCGCGCGCGT AACCTGCGCG GCACGCGCGT AGTTGCGCTG CACCGCTCGG AGCGGTGCGG 720
 TGACACCTTC TTGTTACCGC AGTACCTGTC CAGCAGGAT CCGAGGCGCT GCGGCGAGTC 780
 45 GCGCGCTTC GGCACACCGG TCGACTTCCG GCGGCTGCGG GGTGCGCTCG GTGAGAACCG 840
 CAACGCGCGC ATGGTGACCG GTTGCGCCGA GACACCGCGC TCGTTCGCTT ATATCGCAT 900
 CGCTTCTGTC GACCAAGCGA GTCAACCGCG ACTCGCGCGG GCGCAACTAG GCAATAGCTC 960
 50 TCGCAATTC TTGTTGCGCG AGCGGCAAGC CATTGAGCGG GCGGCGCGTG GCTTGCATTC 1020
 GAAAACCCCG GCGAAGCAGG CCAATTCTAT GATCGAGCGG CCGCGCGCGG AGCGCTACCC 1080
 55 GATCATCAAC TACGAGTACG CCGTGTCTCA CAACGCGCA AAGGACCGCG CCGCGCGCGA 1140
 GACCTTCGAG GCAATTCTGC ACTGCGCGAT CACCGAGCGC AACAGGCGT GGTTCCTCGA 1200
 CCAAGTTCA 1260
 60 GACCAATTTC AGCTAGCTTC GTGACACCG AGCGGACAGC AACCTGCTTC GCGGCATCGG 1320
 GCTGCTTTC GAGAGATGCT GCGCGCTGCG GGTGAGTTC GCGGCGCTCG CCGGCGCATC 1380
 65 CGTTCGCTCG GTGGATAGG TCGGCTGATC CCGCTGCTTC CGCTGCTCTT GGTGCTGCTG 1440
 GTGCTGCTCA TCGAGGCGAT GGTGCGATC AGCTGCAAGC GGTTCGATTT GTTACCGCGC 1500

ACCGAAATGGA ATCCAGGCAA CAGCTACGGC GAAACGGTTC TCACCGACGC GTGCGCCATC 1560
 CGGTGCGGCG CTAATAAGCG GGTTCGGCGC TGATCTGCGC GACGCTGGCG ACCGCGGCAA 1620
 5 TCGCCCTGAT CATCGCGGTG CGGTCTCTTC TAGGAGCGGC GTTGTGTGAT CTGGAACGGC 1680
 TCGCGAAGAG GTTGGCGGAG GCTGTGGGAA TAGTCTGGA ATTCTCTGCT GGAATCCCA 1740
 10 GGTGTGTGAT CGTTTGTGCG GCGCAATGA CTTTCGGCGC GTTCTGTGCT CATCACATCG 1800
 CTCGGTGTAT CGCTCACAC GCTCCGATG TCGCTGTCT GAACTACTTG CCGCGCGAC 1860
 CCGGCAACCG GAGGGGCTG TTGCTGTGCG GTCTGTGTT GCGCTGTGCG GTCTGTGCG 1920
 15 TTATCGGAC CAGACTCAT GAGCTGTGCG GCGAGTGGC GTTGTGCGC CCGGAGGCG 1980
 CGATCGGGA TTC 1993

20 (2) INFORMATION FOR SEQ ID NO:39: 38 kD

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 374 amino acids
 (B) TYPE: amino acid
 25 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:39:

30 Met Lys Ile Arg Leu His Thr Leu Leu Ala Val Leu Thr Ala Ala Pro
 1 5 10 15
 Leu Leu Leu Ala Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser
 20 25 30
 35 Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
 35 40 45
 Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
 40 50 55 60
 Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
 65 70 75 80
 45 Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
 85 90 95
 Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
 100 105 110
 50 Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser
 115 120 125
 Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys
 130 135 140
 55 Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr
 145 150 155
 60 Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro
 160 165 170 175
 Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr
 180 185 190
 65 Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly
 195 200 205

Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly
 210 215 220
 5 Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu
 225 230 235 240
 Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala
 245 250 255
 10 Ser Gln Arg Gly Leu Gly Glu Ala Glu Leu Gly Asn Ser Ser Gly Asn
 260 265 270
 Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala Gly Phe
 275 280 285
 15 Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro
 290 295 300
 20 Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn
 305 310 315 320
 Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu
 325 330 335
 25 His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val
 340 345 350
 His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
 355 360 365
 30 Ile Ala Thr Ile Ser Ser
 370

35 (2) INFORMATION FOR SEQ ID NO:40: DPEP

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (x1) SEQUENCE DESCRIPTION: SEQ ID NO:40:

45 ATGCATCACC ATCACCATCA CATGCATCAG GTGCACCCCA ACTGCACACG TCGCAAGGGA 60
 CATTGGCGG CACTGGCTAT TCGGGCGATG GCCAGGCTCA GCTTGGTGAC GTTGGGTTG 120
 CCGCGACCG CCAACGCGCA TCGGAGCGCA GCGCCGCGCG TACCCACAAC GCGCGCTCG 180
 CCGCGCTCGA CCGCTGCAGC GCCACCGCGA CCGCGCACAC CTGTTGCCCC CCGACCAACG 240
 GCGCGCGCA ACACGCGGAA TCGCCAGCGG GCGGATCGCA ACCGAGCACT TCGCGCGCGC 300
 50 GACCGCAACG CACCGCGCGC ACCGTGCATT GCGCCAAAGG CACCGCAACG TGTCCGAGTC 360
 GACAAACCGG TGGAGGATT CAGCTTCGCG CTGCGCTGCTG GCTGGGTGGA GTCTGACGCG 420
 GCGCACTTG ACTACGCTC AGCACTCTC AGCAAAACCA CCGCGACCT GCCATTTCCC 480
 GACACGCGC CCGCGCTGC CAGTGCAGC GTTATCGTTC TCGCGCGCT AGACCAAGAG 540
 CTTACGCGA GCGCGAGAG CACCGACTCC AAGCGCGCG GCGGCTGGG CTCGACATG 600
 55 GGTGATTCG ATATGCGTA CCGGGGCGC CGATTCAGC AGGAACCGT CTCGCTCGAC 660
 GCGAAGCGG TGTCTGGAAG CCGCTCTAT TACGAAGTCA AGTTCAGCGA TCGAGTAAAG 720
 CCGAAGCGC AGATCTGAC GCGCTAATC GCGTGGCGG CCGCGAAGC ACCGAGCGC 780
 GCGCGCTCT AGCGTGGTT TGTGATAGG CTCGCGACG CCAACACCC GTTGGCAGG 840
 GCGCGCGCA AGCGCTGCG CCAATCGAT CCGCTTTGG TCGCGCGCG GCGCGCGCG 900
 60 GCACCGCTC CTGCAGAGC GCTCGCGCG CCGCGCGCG CCGCGAAGT CGCTCTAGC 960
 CCGACGACAC CGACACCGCA GCGGACCTA CCGCTTGA 999

65 (2) INFORMATION FOR SEQ ID NO:41: DPEP

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

5 Met His His His His His His Met His Gln Val Asp Pro Asn Leu Thr
1 5 10 15
Arg Arg Lys Gly Arg Leu Ala Ala Leu Ala Ile Ala Ala Met Ala Ser
20 25 30
10 Ala Ser Leu Val Thr Val Ala Val Pro Ala Thr Ala Asn Ala Asp Pro
35 40 45
Glu Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr
50 55 60
15 Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro
65 70 75 80
Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala
85 90 95
Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Val Ile Ala Pro
100 105 110
20 Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser
115 120 125
Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp
130 135 140
25 Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro
145 150 155 160
Gly Gln Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg
165 170 175
Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala
180 185 190
30 Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro
195 200 205
Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val
210 215 220
35 Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys
225 230 235 240
Pro Asn Gly Gln Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Ala Asn
245 250 255
Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp Phe Val Val Trp Leu Gly
260 265 270
40 Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Glu
275 280 285
Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro
290 295 300
45 Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr
305 310 315 320
Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala
325 330

50 (2) INFORMATION FOR SEQ ID NO:42: TMH4

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 782 base pairs
(B) TYPE: nucleic acid
55 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

60 CGGCACGAGG ATCGGTAGCC CCGGCATCC GCACTGCCC ATTCGCCCGG TTTCCCCACC 60
CGAGGAAGC CACTACAGA TGGCTGCG GAAGTAGGCG GATCGTTTCG CGATGCCGCG 120
ATGAACGGC GGCATCAAT TACTCAGGA ACCTTTCGT TTAGCGACA TAATGGCTAT 180
AGCACTAGG AGGATGATC GATATGACC AGTCACGAC CTGACGGTC GATCAACAG 240
AGATTTTGA CAGGICCAAC GAGTGGAGG CCGGATGCG CGACCCACCG ACTGATGTCC 300
65 GCATCACACC GTCCAACTC ACCGCGGTA AAAACGCCC CCACCGGTC GINTGTCCG 360
CGACACAT CGCGAATC CTGGCGGCG GTCCCAAGA GCGCAGCGT CTGCGACCT 420
CGCTGCGCA CCGCGCGAG GGGTATGCG AGGTGATTA CGGCTGCG ACCCGCTCG 480
ACACGACCG CAAAGAACT GTGACGCGG ATCGGCCCG GGCCTCGA GCGACAT 540

CGGCCCAACT AACCGATACG CCGAGGGTGG CCACGGCCGG TGAACCAAC TCATGGATC 500
 TCAAGAGAAC GGCACGAGAG CTCGAAACGG GCGACCAAGG CACATCGCTC GGCATTENG 550
 GGCATGGGTG GAACACTTTC ACCTTACGC TGCAGGGGCA CG 702

5

(2) INFORMATION FOR SEQ ID NO:43: THER4

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 286 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:43:

15

Gly Asp Ser Phe Trp Ala Ala Ala Asp Gln Met Ala Arg Gly Phe Val
 1 5 10 15
 Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln
 20 25 30
 His Ala Asp Gly His Ser Leu Leu Leu Asp Ala Thr Asn Pro Ala Val
 35 40 45
 Val Ala Tyr Asp Pro Ala Phe Ala Tyr Glu Ile Gly Tyr Ile Xaa Glu
 50 55 60
 Ser Gly Leu Ala Arg Met Cys Gly Glu Asn Pro Glu Asn Ile Phe Phe
 65 70 75 80
 Tyr Ile Thr Val Tyr Asn Glu Pro Tyr Val Glu Pro Pro Glu Pro Glu
 85 90 95
 Asn Phe Asp Pro Glu Gly Val Leu Gly Gly Ile Tyr Arg Tyr His Ala
 100 105 110
 Ala Thr Glu Gln Arg Thr Asn Lys Xaa Gln Ile Leu Ala Ser Gly Val
 115 120 125
 Ala Met Pro Ala Ala Leu Arg Ala Ala Gln Met Leu Ala Ala Glu Trp
 130 135 140
 Asp Val Ala Ala Asp Val Trp Ser Val Thr Ser Trp Gly Glu Leu Asn
 145 150 155 160
 Arg Asp Gly Val Val Ile Glu Thr Glu Lys Leu Arg His Pro Asp Arg
 165 170 175
 Pro Ala Gly Val Pro Tyr Val Thr Arg Ala Leu Glu Asn Ala Arg Gly
 180 185 190
 Pro Val Ile Ala Val Ser Asp Trp Met Arg Ala Val Pro Glu Gln Ile
 195 200 205
 Arg Pro Trp Val Pro Gly Thr Tyr Leu Thr Leu Gly Thr Asp Gly Phe
 210 215 220
 Gly Phe Ser Asp Thr Arg Pro Ala Gly Arg Arg Tyr Phe Asn Thr Asp
 225 230 235 240
 Ala Glu Ser Gln Val Gly Arg Gly Phe Gly Arg Gly Trp Pro Gly Arg
 245 250 255
 Arg Val Asn Ile Asp Pro Phe Gly Ala Gly Arg Gly Pro Pro Ala Gln
 260 265 270
 Leu Pro Gly Phe Asp Glu Gly Gly Gly Leu Arg Pro Xaa Lys
 275 280 285

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(2) INFORMATION FOR SEQ ID NO:44: DPFD

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

60

(ii) MOLECULE TYPE: Genomic DNA

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:44:

65

ATGAAGTTGA AGTTTCTCTA CTTAGTACT GGTATCTGG GTGTGCAAG GGCCTTGTG 60
 TTCTCTGCTT CGGTTCCTCG CACAGATCCA CTTACCCGCT ATCAGGCGGA CATGACAAA 120
 GGTATTGCTT CGGTTCCTCG AATGGGTTT GCGACTTGG CATTGTGCGA CAGCAGAAAG 180

```

TACCCCGGACG GCTGCTTTTG GCACCACTGG ATGCAACGCT GCTTTACCGG CCCACAGTTT 240
TACTTCGATT GGTTCAGCGG CGGTGAGCCC CTGCCCCGCC CGCCGECACC GGGTGGTTGC 300
GGTGGGCAAA TTCCGTGCGA GCAGCCCAAC GTCCTCTGA 339

```

5

(2) INFORMATION FOR SEQ ID NO:45: DPED

(i) SEQUENCE CHARACTERISTICS:

10

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(A) LENGTH: 112 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

```

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```

Met Lys Leu Lys Phe Ala Arg Leu Ser Thr Ala Ile Leu Gly Cys Ala
  1           5           10           15
20  Ala Ala Leu Val Phe Pro Ala Ser Val Ala Ser Ala Asp Pro Pro Asp
    20           25           30
    Pro His Gln Pro Asp Met Thr Lys Gly Tyr Cys Pro Gly Gly Arg Trp
    35           40           45
25  Gly Phe Gly Asp Leu Ala Val Cys Asp Gly Glu Lys Tyr Pro Asp Gly
    50           55           60
    Ser Phe Trp His Gln Trp Met Gln Thr Trp Phe Thr Gly Pro Gln Phe
    65           70           75           80
    Tyr Phe Asp Cys Val Ser Gly Gly Glu Pro Leu Pro Gly Pro Pro Pro
    85           90           95
30  Pro Gly Gly Cys Gly Gly Ala Ile Pro Ser Gln Gln Pro Asn Ala Pro
    100           105           110

```

```

<210> SEQ ID NO:46
35  <211> 333
    <212> DNA
    <213> Artificial Sequence
    <223> Description of Artificial Sequence: tri-fusion
        protein DPV-MPI-MSL (designated Mtb31f)
40  <323> (1) .. (300)

```

```

cat atg cat cac cat cac cat cac gat ccc gtg gac gog gtc att aac 48
His Met His His His His His Asp Pro Val Asp Ala Val Ile Asn
  1           5           10           15
45  acc acc tgc aat tac ggg cag gta gta got gog ctc aac gog aog gat 96
Thr Thr Cys Asn Tyr Gly Gln Val Val Ala Ala Leu Asn Ala Thr Asp
    20           25           30
50  cgg ggg got ggc gca cag ttc aac gcc toa cgg gtg gog cag tcc tat 144
Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser Pro Val Ala Gln Ser Tyr
    35           40           45
55  ttg cgc aat ttc ctc gcc gca ccg cca cct cag cgc gct gcc atg gcc 192
Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro Gln Arg Ala Ala Met Ala
    50           55           60
60  gog caa ttg caa got gtg cgg ggg gog gca cag tac atc ggc ctt gtc 240
Ala Gln Leu Gln Ala Val Pro Gly Ala Ala Gln Tyr Ile Gly Leu Val
    65           70           75           80
    gag tgg gtt gcc ggc tcc tgc aac aac tat gag ctc atg aog att aat 288
Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr Glu Leu Met Thr Ile Asn
    85           90           95
65  tac cag ttc ggg gac gtc gac got cat ggc gcc atg atc cgc got cag 336
Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln
    100           105           110

```

gag gag tog ctt gag gag gag cat gag gcc atc ggt cgt gat gag ttg 384
 Ala Ala Ser Leu Glu Ala Glu His Glu Ala Ile Val Arg Asp Val Leu
 115 120 125
 5 gcc gag ggt gac ttt tgg ggc gcc gcc ggt tog gtg gct tgc cag gag 432
 Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Glu
 130 135 140
 10 ttc att acc cag ttg ggc cgt aac ttc cag gtg atc tac gag cag gcc 480
 Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile Tyr Glu Gln Ala
 145 150 155 160
 15 aac gcc cac gag cag aag gtg cag gct gcc gcc aac aac atg gag caa 528
 Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn Asn Met Ala Gln
 165 170 175
 20 acc gac agc gcc gtc ggc tcc agc tgg gcc act agt atg agc ctt ttg 576
 Thr Asp Ser Ala Val Gly Ser Ser Trp Ala Thr Ser Met Ser Leu Leu
 180 185 190
 25 gat gct cat atc cca cag ttg gtg gcc tcc cag tog gag ttt gcc gcc 624
 Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala
 195 200 205
 aag gag ggg ctg atg cgg cag acg atc ggt cag gcc gag cag gag gag 672
 Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala Glu Gln Ala Ala
 210 215 220
 30 atg tog gct cag gag ttt cac cag ggg gag tog tog gag gag ttt cag 720
 Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser Ala Ala Phe Gln
 225 230 235 240
 35 gcc gcc cat gcc cgg ttt gtg gag gag gcc gcc aac gtc aac acc ttg 768
 Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys Val Asn Thr Leu
 245 250 255
 40 ttg gat gtc gag cag gag aat ctg ggt gag gcc gcc ggt acc cat gtg 816
 Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val
 260 265 270
 gcc gcc gat gct gag gcc gag tog acc tat acc gag ttc gat atc cat 864
 Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Gly Phe Asp Ile His
 275 280 285
 45 car act gcc gcc cgc tog agc aga tcc gcc tgc taaacaaagcc cgaagaggag 917
 His Thr Gly Gly Arg Ser Ser Arg Ser Gly Cys
 290 295
 50 ctga 921

55 <210> SEQ ID NO:47
 <211> 399
 <212> PRT
 <213> Artificial Sequence
 <214> Description of Artificial Sequence: tri-fusion
 protein DPV-MPI-MEL (designated Mtblif)

60 His Met His His His His His His Asp Pro Val Asp Ala Val Ile Asn
 1 5 10 15
 Thr Thr Cys Asn Tyr Gly Glu Val Val Ala Ala Leu Asn Ala Thr Asp
 20 25 30
 65 Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser Pro Val Ala Gln Ser Tyr
 35 40 45

Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro Gln Arg Ala Ala Met Ala
 55 55 60
 5 Ala Gln Leu Gln Ala Val Pro Gly Ala Ala Gln Tyr Ile Gly Leu Val
 65 70 75
 Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr Glu Leu Met Thr Ile Asn
 85 90 95
 10 Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln
 100 105 110
 Ala Ala Ser Leu Gln Ala Gln His Gln Ala Ile Val Arg Asp Val Leu
 115 120 125
 15 Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Glu
 130 135 140
 20 Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile Tyr Glu Gln Ala
 145 150 155 160
 Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn Asn Met Ala Gln
 165 170 175
 25 Thr Asp Ser Ala Val Gly Ser Ser Trp Ala Thr Ser Met Ser Leu Leu
 180 185 190
 Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala
 195 200 205
 30 Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala Glu Gln Ala Ala
 210 215 220
 35 Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser Ala Ala Phe Gln
 225 230 235 240
 Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys Val Asn Thr Leu
 245 250 255
 40 Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val
 260 265 270
 Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Gly Phe Asp Ile His
 275 280 285
 45 His Thr Gly Gly Arg Ser Ser Arg Ser Gly Cys
 290 295
 50 <210> SEQ ID NO:48
 <211> 3168
 <212> DNA
 <213> Artificial Sequence
 <223> Description of Artificial Sequence:tetra-fusion
 55 protein DPV-MTI-MSL-MTCC2 (designated Mtb71f)
 <323> (1)..(3133)
 cat atg cat cac cat cac cat cac gat ccc gtg gac gcg gtc att aac 48
 60 His Met His His His His His Asp Pro Val Asp Ala Val Ile Asn
 1 5 10 15
 aac acc tgc aat tac ggg cag gta gta got gcg ctc aac gcg acg gat 96
 Thr Thr Cys Asn Tyr Gly Gln Val Val Ala Ala Leu Asn Ala Thr Asp
 20 25 30
 65 cag ggg got gcc gca cag ttc aac gcc tca cag gtg gcg cag tcc tat 144
 Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser Pro Val Ala Gln Ser Tyr
 35 40 45

5	ttg agc aat ttc ctg gcc gaa cag cca cct cag agc ggt gcc atg gcc	192
	Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro Gln Arg Ala Ala Met Ala	
10	ggc caa ttg caa ggt gtg ccg ggg ggg gca cag tac atc ggc ctt gtc	240
	Ala Gln Leu Gln Ala Val Pro Gly Ala Ala Gln Tyr Ile Gly Leu Val	
15	gag tgg gtc gcc ggc tcc tgc aac aac tat gag ctg atg aag att aat	288
	Gly Ser Val Ala Gly Ser Cys Asn Asn Tyr Gln Leu Met Thr Ile Asn	
20	tac cag ttc ggg gac gtc gac ggt cat ggc gcc atg atc ggc ggt cag	336
	Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln	
25	ggc ggc tgg ctt gag ggc gag cat cag gcc atc gtc cgt gat gtg ttg	384
	Ala Ala Ser Leu Gln Ala Gln His Gln Ala Ile Val Arg Asp Val Leu	
30	ggc ggc ggt gac ttc tgg ggc ggc gcc ggt tgg gtg ggt tgc cag gag	432
	Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Gln	
35	ttc att acc cag ttg ggc cgt aac ttc cag gtg atc tac gag cag gcc	480
	Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile Tyr Gln Gln Ala	
40	aac gcc cac ggg cag aag gtg cag ggt gcc ggc aac aac atg gag caa	528
	Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn Asn Met Ala Gln	
45	acc gac agc gcc gtc ggc tcc agc tgg gcc act agt atg agc ctt ttg	576
	Thr Asp Ser Ala Val Gly Ser Ser Trp Ala Thr Ser Met Ser Leu Leu	
50	gat gct cat atc cca cag ttg gtg gcc tcc cag tgg ggc ttt gcc gcc	624
	Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala	
55	aag gag ggg ctg atg cgg cac acg atc ggt cag gcc gag cag gag gcc	672
	Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala Gln Gln Ala Ala	
60	atg tgg ggt cag ggc ttt cac cag ggg gag tgg ggc gag ttt cag	720
	Met Ser Ala Gln Ala Phe His Gln Gly Gln Ser Ser Ala Ala Phe Gln	
65	gcc gcc cat gcc cgg ttt gtg ggc gcc gcc gcc aac gtc aac acc ttg	768
	Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys Val Asn Thr Leu	
70	ttg gat gtc ggc cag ggc aat ctg ggt gag gcc gcc ggt acc tat gtg	816
	Leu Asp Val Ala Gln Ala Asn Leu Gly Gln Ala Ala Gly Thr Tyr Val	
75	gcc gcc gat ggt ggc gcc ggc tgg acc tat acc ggg ttc gat atc atg	864
	Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Gly Phe Asp Ile Met	
80	gat ttc ggg ctt tta cct ccg gaa gtg aat tca agc cga atg tat tcc	912
	Asp Phe Gly Leu Leu Pro Pro Gln Val Asn Ser Ser Arg Met Tyr Ser	
85	ggc cgg ggg ccg gag tgg atg cta gcc gcc ggc gcc gcc tgg gac ggt	960
	Gly Pro Gly Pro Gln Ser Met Leu Ala Ala Ala Ala Trp Asp Gly	

5	gtg gcc gcg gag atg act tcc gcc gcg gtc tgg tat gga tgg gtg gtg	1000
	Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val Val	
10	tcg acg ctg atc gtt gag ccg tgg atg ggg ccg gcg gcg gcc gcg atg	1056
	Ser Thr Leu Ile Val Glu Pro Trp Met Gly Pro Ala Ala Ala Met	
15	ggg gcc gcg gca acg ccg tat gtg ggg tgg ctg gcc gcc acg gcg gcg	1104
	Ala Ala Ala Ala Thr Pro Tyr Val Gly Trp Leu Ala Ala Thr Ala Ala	
20	ctg gcg aag gag acg gcc acc cag gcg agg gca gcg gcg gaa gcg ttc	1152
	Leu Ala Lys Glu Thr Ala Thr Gln Ala Arg Ala Ala Ala Glu Ala Phe	
25	ggg acg gcg ttc gcg atg acg gtg cca cca tcc ctg gtc gcg gcc aac	1200
	Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala Asn	
30	agg acg ccg ttg atg tgg ctg gtc gcg gcg aac att ctg ggg cca aac	1248
	Arg Ser Arg Leu Met Ser Leu Val Ala Ala Asn Ile Leu Gly Gln Asn	
35	agt gcg gcg atc gcg gct acc cag gcc gag tat gcc gaa atg tgg gcc	1296
	Ser Ala Ala Ile Ala Ala Thr Gln Ala Glu Tyr Ala Glu Met Trp Ala	
40	caa gac gct gcc gtg atg tac agc tat gag ggg gca tct gcg gcc gcg	1344
	Gln Asp Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala Ala	
45	tgg gcg ttg ccg ccg ttc act cca ccc gtg cca ggc acc ggc ccg gcc	1392
	Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Gln Gly Thr Gly Pro Ala	
50	ggg ccc gcg gcc gca gcc gcg gcy acc cca gcc gcc ggt gcg ggc gcc	1440
	Gly Pro Ala Ala Ala Ala Ala Thr Gln Ala Ala Gly Ala Gly Ala	
55	gtt gcg gat gca cag gcg acc ctg gcc cag ctg ccc ccg ggg atc ctg	1488
	Val Ala Asp Ala Gln Ala Thr Leu Ala Gln Leu Pro Pro Gly Ile Leu	
60	agc gac att ctg tcc gca ttg gcc gcc aac gct gat ccg ctg acc tgg	1536
	Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr Ser	
65	gga ctg ttg ggg atc gcg tgg acc ctg aac ccg cca gtc gga tcc gct	1584
	Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gln Val Gly Ser Ala	
70	cag ccg ata gtg atc ccc acc ccg ata ggg gaa ttg gac gtg atc gcg	1632
	Gln Pro Ile Val Ile Pro Thr Pro Ile Gly Glu Leu Asp Val Ile Ala	
75	ctc tcc att gca tcc atc gcg acc ggc agc att gcg ctg gcg atc acg	1680
	Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile Thr	
80	aac acg gcc aga ccc tgg ccc atc ggc cta tac ggg aac gcc ggc ggg	1728
	Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly Gly	
85	ctg gga ccg acg cag gcc cat cca ctg agt tgg gcg acc gac gag ccg	1776
	Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu Pro	

5	gag cag cac tgg ggc ccc ttc ggg ggc ggc ggc cag gtg tcc ggc ggc	1824
	Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala Gly	
10	gtc ggc ccc gca gca tta gtc gga ggc ttg tgg gtg cag cac agc tgg	1872
	Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser Trp	
15	acc acg gcc gcc ccg gag atc cag ctc gcc gtt cag gca aca ccc acc	1920
	Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro Thr	
20	ctc agc tcc agc gcc ggc gcc gac ccg acg gcc cta aac ggc atg ccg	1968
	Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met Pro	
25	gca ggc ctg ctc agc ggc atg gct ttg ggc agc ctg gcc gca cgc ggc	2016
	Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg Gly	
30	acg acg ggc ggt ggc ggc acc cgt agc ggc acc agc act gac ggc caa	2064
	Thr Thr Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly Gln	
35	gag gac ggc cgc aca ccc ccg gta gtt gtg att aga gag cag ccg ccg	2112
	Glu Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Gln Gln Pro Pro	
40	ccc gga aac ccc ccg cgg taagattttct aattccatcca caatgggggc cgtctgag	2160
	Pro Gly Asn Pro Pro Arg	
45	<210> SEQ ID NO:49	
	<211> 710	
50	<212> PRT	
	<213> Artificial Sequence	
55	<221> Description of Artificial Sequence: Tetra-fusion	
	protein GPV-MTI-MSE-MTCC2 (designated Mub71f)	
60	His Met His His His His His Asp Pro Val Asp Ala Val Ile Asn	
	1 5 10 15	
65	Thr Thr Cys Asn Tyr Gly Gln Val Val Ala Ala Leu Asn Ala Thr Asp	
	20 25 30	
70	Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser Pro Val Ala Gln Ser Tyr	
	35 40 45	
75	Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro Gln Arg Ala Ala Met Ala	
	50 55 60	
80	Ala Gln Leu Gln Ala Val Pro Gly Ala Ala Gln Tyr Ile Gly Leu Val	
	65 70 75 80	
85	Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr Glu Leu Met Thr Ile Asn	
	85 90 95	
90	Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln	
	100 105 110	
95	Ala Ala Ser Leu Glu Ala Glu His Gln Ala Ile Val Arg Asp Val Leu	
	115 120 125	
100	Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Glu	
	130 135 140	

	Phe	Ile	Thr	Gln	Leu	Gly	Arg	Asn	Phe	Gln	Val	Ile	Tyr	Glu	Gln	Ala	
	148					150					155					160	
5	Asn	Ala	His	Gly	Gln	Lys	Val	Gln	Ala	Ala	Gly	Asn	Asn	Met	Ala	Gln	
				165						170						175	
	Thr	Asp	Ser	Ala	Val	Gly	Ser	Ser	Trp	Ala	Thr	Ser	Met	Ser	Leu	Leu	
				180					185					190			
10	Asp	Ala	His	Ile	Pro	Gln	Leu	Val	Ala	Ser	Gln	Ser	Ala	Phe	Ala	Ala	
			195					200					205				
	Lys	Ala	Gly	Leu	Met	Arg	His	Thr	Ile	Gly	Gln	Ala	Gln	Gln	Ala	Ala	
	210					215						220					
15	Met	Ser	Ala	Gln	Ala	Phe	His	Gln	Gly	Glu	Ser	Ser	Ala	Ala	Phe	Gln	
	225					230					235					240	
	Ala	Ala	His	Ala	Arg	Phe	Val	Ala	Ala	Ala	Ala	Lys	Val	Asn	Thr	Leu	
20				245						250					255		
	Leu	Asp	Val	Ala	Gln	Ala	Asn	Leu	Gly	Gln	Ala	Ala	Gly	Thr	Tyr	Val	
			260					265						270			
25	Ala	Ala	Asp	Ala	Ala	Ala	Ala	Ser	Thr	Tyr	Thr	Gly	Phe	Asp	Ile	Met	
			275					280					285				
	Asp	Phe	Gly	Leu	Leu	Pro	Pro	Glu	Val	Asn	Ser	Ser	Arg	Met	Tyr	Ser	
	290					295						300					
30	Gly	Pro	Gly	Pro	Glu	Ser	Met	Leu	Ala	Ala	Ala	Ala	Ala	Trp	Asp	Gly	
	305					310					315					320	
	Val	Ala	Ala	Glu	Leu	Thr	Ser	Ala	Ala	Val	Ser	Tyr	Gly	Ser	Val	Val	
				325						330					335		
35	Ser	Thr	Leu	Ile	Val	Glu	Pro	Trp	Met	Gly	Pro	Ala	Ala	Ala	Ala	Met	
			340					345						350			
	Ala	Ala	Ala	Ala	Thr	Pro	Tyr	Val	Gly	Trp	Leu	Ala	Ala	Thr	Ala	Ala	
40			355				360						365				
	Leu	Ala	Lys	Glu	Thr	Ala	Thr	Gln	Ala	Arg	Ala	Ala	Ala	Glu	Ala	Phe	
	370					375					380						
45	Gly	Thr	Ala	Phe	Ala	Met	Thr	Val	Pro	Pro	Ser	Leu	Val	Ala	Ala	Asn	
	385					390					395					400	
	Arg	Ser	Arg	Leu	Met	Ser	Leu	Val	Ala	Ala	Asn	Ile	Leu	Gly	Gln	Asn	
				405						410					415		
50	Ser	Ala	Ala	Ile	Ala	Ala	Thr	Gln	Ala	Glu	Tyr	Ala	Glu	Met	Trp	Ala	
			420					425						430			
	Gln	Asp	Ala	Ala	Val	Met	Tyr	Ser	Tyr	Gln	Gly	Ala	Ser	Ala	Ala	Ala	
55			435				440						445				
	Ser	Ala	Leu	Pro	Pro	Phe	Thr	Pro	Pro	Val	Gln	Gly	Thr	Gly	Pro	Ala	
			450				455					460					
60	Gly	Pro	Ala	Ala	Ala	Ala	Ala	Ala	Thr	Gln	Ala	Ala	Gly	Ala	Gly	Ala	
	465					470					475					480	
	Val	Ala	Asp	Ala	Gln	Ala	Thr	Leu	Ala	Gln	Leu	Pro	Pro	Gly	Ile	Leu	
				485						490					495		
65	Ser	Asp	Ile	Leu	Ser	Ala	Leu	Ala	Ala	Asn	Ala	Asp	Pro	Leu	Thr	Ser	
				500					505					510			

Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gln Val Gly Ser Ala
 518 520 525
 5 Gln Pro Ile Val Ile Pro Thr Pro Ile Gly Glu Leu Asp Val Ile Ala
 530 535 540
 Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile Thr
 545 550 555 560
 10 Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly Gly
 565 570 575
 Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu Pro
 580 585 590
 15 Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala Gly
 595 600 605
 20 Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser Trp
 610 615 620
 Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro Thr
 625 630 635 640
 25 Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met Pro
 645 650 655
 Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg Gly
 660 665 670
 30 Thr Thr Gly Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly Gln
 675 680 685
 35 Glu Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Glu Gln Pro Pro
 690 695 700
 Pro Gly Asn Pro Pro Arg
 705 710
 40